

# SEQUENCE LISTING

<110> Reznikoff, William S.  
Steiniger-White, Mindy M.  
Metzler, Jeremy

<120> Tn5 Transposase Mutants And The Use Thereof

<130> 960296.99195

<150> 60/463,470

<151> 2003-04-17

<160> 5

<170> PatentIn version 3.2

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<213> Transposon Tn5

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ttc tct tcg gcg gcg ctg ggt gat cct cgc cgt act gcc cgc ttg gtt	96
Phe Ser Ser Ala Ala Leu Gly Asp Pro Arg Arg Thr Ala Arg Leu Val	
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aac gtc gcc gcc caa ttg gca aaa tat tct ggt aaa tca ata acc atc	144
Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile	
35 40 45	
tca tca gag ggt agt gaa gcc atg cag gaa ggc gct tac cga ttt atc	192
Ser Ser Glu Gly Ser Glu Ala Met Gln Glu Gly Ala Tyr Arg Phe Ile	
50 55 60	
cgc aat ccc aac gtt tct gcc gag gcg atc aga aag gct ggc gcc atg	240
Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met	
65 70 75 80	
caa aca gtc aag ttg gct cag gag ttt ccc gaa ctg ctg gcc att gag	288
Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu	
85 90 95	
gac acc acc tct ttg agt tat cgc cac cag gtc gcc gaa gag ctt ggc	336
Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly	
100 105 110	
aag ctg ggc tct att cag gat aaa tcc cgc gga tgg tgg gtt cac tcc	384
Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser	
115 120 125	
gtt ctc ttg ctc gag gcc acc aca ttc cgc acc gta gga tta ctg cat	432

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cag	gag	tgg	tgg	atg	cgc	ccg	gat	gac	cct	gcc	gat	gcg	gat	gaa	aag	480	
Gln	Glu	Trp	Trp	Met	Arg	Pro	Asp	Asp	Pro	Ala	Asp	Ala	Asp	Glu	Lys		
145					150					155					160		
gag	agt	ggc	aaa	tgg	ctg	gca	gcg	gcc	gca	act	agc	cgg	tta	cgc	atg	528	
Glu	Ser	Gly	Lys	Trp	Leu	Ala	Ala	Ala	Ala	Thr	Ser	Arg	Leu	Arg	Met		
				165					170					175			
ggc	agc	atg	atg	agc	aac	gtg	att	gcg	gtc	tgt	gac	cgc	gaa	gcc	gat	576	
Gly	Ser	Met	Met	Ser	Asn	Val	Ile	Ala	Val	Cys	Asp	Arg	Glu	Ala	Asp		
			180					185					190				
att	cat	gct	tat	ctg	cag	gac	aaa	ctg	gcg	cat	aac	gag	cgc	ttc	gtg	624	
Ile	His	Ala	Tyr	Leu	Gln	Asp	Lys	Leu	Ala	His	Asn	Glu	Arg	Phe	Val		
		195					200					205					
gtg	cgc	tcc	aag	cac	cca	cgc	aag	gac	gta	gag	tct	ggg	ttg	tat	ctg	672	
Val	Arg	Ser	Lys	His	Pro	Arg	Lys	Asp	Val	Glu	Ser	Gly	Leu	Tyr	Leu		
	210					215					220						
tac	gac	cat	ctg	aag	aac	caa	ccg	gag	ttg	ggg	ggc	tat	cag	atc	agc	720	
Tyr	Asp	His	Leu	Lys	Asn	Gln	Pro	Glu	Leu	Gly	Gly	Tyr	Gln	Ile	Ser		
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att	ccg	caa	aag	ggc	gtg	gtg	gat	aaa	cgc	ggg	aaa	cgt	aaa	aat	cga	768	
Ile	Pro	Gln	Lys	Gly	Val	Val	Asp	Lys	Arg	Gly	Lys	Arg	Lys	Asn	Arg		
				245				250						255			
cca	gcc	cgc	aag	gcg	agc	ttg	agc	ctg	cgc	agt	ggg	cgc	atc	acg	cta	816	
Pro	Ala	Arg	Lys	Ala	Ser	Leu	Ser	Leu	Arg	Ser	Gly	Arg	Ile	Thr	Leu		
			260					265					270				
aaa	cag	ggg	aat	atc	acg	ctc	aac	gcg	gtg	ctg	gcc	gag	gag	att	aac	864	
Lys	Gln	Gly	Asn	Ile	Thr	Leu	Asn	Ala	Val	Leu	Ala	Glu	Glu	Ile	Asn		
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ccg	ccc	aag	ggg	gag	acc	ccg	ttg	aaa	tgg	ttg	ttg	ctg	acc	agc	gaa	912	
Pro	Pro	Lys	Gly	Glu	Thr	Pro	Leu	Lys	Trp	Leu	Leu	Leu	Thr	Ser	Glu		
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Pro	Val	Glu	Ser	Leu	Ala	Gln	Ala	Leu	Arg	Val	Ile	Asp	Ile	Tyr	Thr		
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cat	cgc	tgg	cgg	atc	gag	gag	ttc	cat	aag	gca	tgg	aaa	acc	gga	gca	1008	
His	Arg	Trp	Arg	Ile	Glu	Glu	Phe	His	Lys	Ala	Trp	Lys	Thr	Gly	Ala		
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gga	gcc	gag	agg	caa	cgc	atg	gag	gag	ccg	gat	aat	ctg	gag	cgg	atg	1056	
Gly	Ala	Glu	Arg	Gln	Arg	Met	Glu	Glu	Pro	Asp	Asn	Leu	Glu	Arg	Met		
			340					345					350				
gtc	tcg	atc	ctc	tcg	ttt	gtt	gcg	gtc	agg	ctg	tta	cag	ctc	aga	gaa	1104	
Val	Ser	Ile	Leu	Ser	Phe	Val	Ala	Val	Arg	Leu	Leu	Gln	Leu	Arg	Glu		
		355					360					365					
agc	ttc	acg	ctg	ccg	caa	gca	ctc	agg	gcg	caa	ggg	ctg	cta	aag	gaa	1152	
Ser	Phe	Thr	Leu	Pro	Gln	Ala	Leu	Arg	Ala	Gln	Gly	Leu	Leu	Lys	Glu		

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gcg gaa cac gta gaa agc cag tcc gca gaa acg gtg ctg acc ccg gat			1200
Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp			
385	390	395	400
gaa tgt cag cta ctg ggc tat ctg gac aag gga aaa cgc aag cgc aaa			1248
Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys			
	405	410	415
gag aaa gca ggt agc ttg cag tgg gct tac atg gcg ata gct aga ctg			1296
Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu			
	420	425	430
ggc ggt ttt atg gac agc aag cga acc gga att gcc agc tgg ggc gcc			1344
Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala			
	435	440	445
ctc tgg gaa ggt tgg gaa gcc ctg caa agt aaa ctg gat ggc ttt ctt			1392
Leu Trp Glu Gly Trp Glu Ala Leu Gln Ser Lys Leu Asp Gly Phe Leu			
	450	455	460
gcc gcc aag gat ctg atg gcg cag ggg atc aag atc tga			1431
Ala Ala Lys Asp Leu Met Ala Gln Gly Ile Lys Ile			
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Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile			
	35	40	45
Ser Ser Glu Gly Ser Glu Ala Met Gln Glu Gly Ala Tyr Arg Phe Ile			
	50	55	60
Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met			
65	70	75	80
Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu			
	85	90	95
Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly			
	100	105	110

Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser  
 115 120 125

Val Leu Leu Leu Glu Ala Thr Thr Phe Arg Thr Val Gly Leu Leu His  
 130 135 140

Gln Glu Trp Trp Met Arg Pro Asp Asp Pro Ala Asp Ala Asp Glu Lys  
 145 150 155 160

Glu Ser Gly Lys Trp Leu Ala Ala Ala Ala Thr Ser Arg Leu Arg Met  
 165 170 175

Gly Ser Met Met Ser Asn Val Ile Ala Val Cys Asp Arg Glu Ala Asp  
 180 185 190

Ile His Ala Tyr Leu Gln Asp Lys Leu Ala His Asn Glu Arg Phe Val  
 195 200 205

Val Arg Ser Lys His Pro Arg Lys Asp Val Glu Ser Gly Leu Tyr Leu  
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Tyr Asp His Leu Lys Asn Gln Pro Glu Leu Gly Gly Tyr Gln Ile Ser  
 225 230 235 240

Ile Pro Gln Lys Gly Val Val Asp Lys Arg Gly Lys Arg Lys Asn Arg  
 245 250 255

Pro Ala Arg Lys Ala Ser Leu Ser Leu Arg Ser Gly Arg Ile Thr Leu  
 260 265 270

Lys Gln Gly Asn Ile Thr Leu Asn Ala Val Leu Ala Glu Glu Ile Asn  
 275 280 285

Pro Pro Lys Gly Glu Thr Pro Leu Lys Trp Leu Leu Leu Thr Ser Glu  
 290 295 300

Pro Val Glu Ser Leu Ala Gln Ala Leu Arg Val Ile Asp Ile Tyr Thr  
 305 310 315 320

His Arg Trp Arg Ile Glu Glu Phe His Lys Ala Trp Lys Thr Gly Ala  
 325 330 335

Gly Ala Glu Arg Gln Arg Met Glu Glu Pro Asp Asn Leu Glu Arg Met  
 340 345 350

Val Ser Ile Leu Ser Phe Val Ala Val Arg Leu Leu Gln Leu Arg Glu  
 355 360 365

Ser Phe Thr Leu Pro Gln Ala Leu Arg Ala Gln Gly Leu Leu Lys Glu  
 370 375 380

Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp  
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Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys  
 405 410 415

Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu  
 420 425 430

Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala  
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